



SEQUENCE LISTING

<110> Haruo HANAWA

<120> VECTOR FOR GENE THERAPY AND METHOD OF QUANTIFYING TARGET PROTEIN IN MAMMAL OR CULTURED CELLS WITH THE ADMINISTRATION OF THE VECTOR FOR GENE THERAPY

<130> 0760-0347PUS1

<140> US 10/541,626

<141> 2005-07-07

<150> PCT/JP2003/016956

<151> 2003-12-26

<150> JP 2003-3967

<151> 2003-01-10

<160> 24

<210> 1

<211> 11

<212> PRT

<213> Artificial Sequence

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<223> oligopeptide encoding C19-29 region of glucagon of human, mouse or rat

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<212> DNA

<213> Artificial Sequence

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<223> DNA insert encoding rat IFN-r receptor, rat IgG Fc region and glucagon C19-29 region

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<222> (13)..(1461)

<223> DNA insert encoding rat IFN-r receptor, rat IgG Fc region and glucagon C19-29 region

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Pro Ala Pro Thr Asn Val Leu Ile Thr Ser Tyr Asp Leu Asn Pro Val			
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gta cat tgg aag cac cag aac gtg tcg cag gct gcc gtc ttc act gta			195
Val His Trp Lys His Gln Asn Val Ser Gln Ala Ala Val Phe Thr Val			
50	55	60	
cag gta aag atg tat cca gaa tac tgg act gat gcc tgc acc aac att			243
Gln Val Lys Met Tyr Pro Glu Tyr Trp Thr Asp Ala Cys Thr Asn Ile			
65	70	75	
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Ala His His Tyr Cys Asn Ile Tyr Lys His Ile Ser Tyr Pro Asp Ser			
80	85	90	
tct gcc tgg gcc aga gtt aag gcc aag gtt gga caa aga gaa tct gcc			339
Ser Ala Trp Ala Arg Val Lys Ala Lys Val Gly Gln Arg Glu Ser Ala			
95	100	105	
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Tyr Ala Gln Ser Glu Glu Phe Ile Met Cys Arg Lys Gly Lys Val Gly			
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ccg cct ggc ctg gac atc gga agg aag gaa gat cag ctg att gtc cac			435
Pro Pro Gly Leu Asp Ile Gly Arg Lys Glu Asp Gln Leu Ile Val His			
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Ile Phe His Pro Lys Val Asn Val Ser Gln Glu Thr Met Phe Gly Asp			
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Gly Asn Thr Cys Tyr Thr Phe Asp Tyr Thr Val Phe Val Lys His Tyr			
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Cys Ser Glu Thr Leu Cys Glu Leu Asn Ile Ser Val Ser Thr Leu Asn			
190	195	200	205
tcc aat tac tgt gtt tca gta gtt gga aag tcg tct ttc tgg caa gtt			675
Ser Asn Tyr Cys Val Ser Val Val Gly Lys Ser Ser Phe Trp Gln Val			
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Asn Thr Glu Thr Ser Lys Asp Ala Cys Ile Pro Phe Leu His Asp Asp			
225	230	235	
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Arg Glu Glu Ala Ala Val Pro Arg Asn Cys Gly Gly Asp Cys Lys			

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cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag gtc acg Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr			867
270	275	280	285
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290	295	300	
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305	310	315	
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320	325	330	
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370	375	380	
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415	420	425	
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430	435	440	445
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 Gln Leu Pro Ser Arg Thr Trp Pro Phe Gly Val Leu Leu Ser Leu Leu
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 Phe Ile Pro Ile Phe Ser Glu Ala Ile Gln Val Thr Gln Pro Ser Val
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 Val Leu Ala Ser Ser His Gly Val Ala Ser Phe Pro Cys Glu Tyr Ala
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 Ser Ser His Asn Thr Asp Glu Val Arg Val Thr Val Leu Arg Gln Thr
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 Asn Asp Gln Val Thr Glu Val Cys Ala Thr Thr Phe Thr Val Lys Asn
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 Thr Leu Gly Phe Leu Asp Asp Pro Phe Cys Ser Gly Thr Phe Asn Glu
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Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His		
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Ser Ser Cys Asn Ala Ile His Arg Thr Gln Arg Ile Leu Asn Gly Leu		
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tgt aac caa aag gcc tcg gat gtg gct tcc agc ccc cca gat acc aaa		339
Cys Asn Gln Lys Ala Ser Asp Val Ala Ser Ser Pro Pro Asp Thr Lys		
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Lys Val Thr Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val			
175	180	185	
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His Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr			
190	195	200	205
cga cca cca gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa			675
Arg Pro Pro Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu			
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Leu Pro Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys			
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acc aag gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta			867
Thr Lys Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val			
270	275	280	285
aaa ggc ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg			915
Lys Gly Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly			
290	295	300	
cag cca cag gaa aac tac aag aac act cca cct acg atg gac aca gat			963
Gln Pro Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp			
305	310	315	
ggg agt tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg			1011
Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp			
320	325	330	
cag cag gga aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac			1059
Gln Gln Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His			

335	340	345	
aac cac cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln 350	355	360	365
gat ttt gtg cag tgg ttg atg aat acc tgagaattc Asp Phe Val Gln Trp Leu Met Asn Thr 370			1107
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gct ctg ggt gta ctg gca ccc tgg agt gtg gaa gga gcg gcc gcc gtg Ala Leu Gly Val Leu Ala Pro Trp Ser Val Glu Gly Ala Ala Ala Val 15 20 25			99
ccc aga aac tgt gga ggt gat tgc aag cct tgt ata tgt aca ggc tca Pro Arg Asn Cys Gly Gly Asp Cys Lys Pro Cys Ile Cys Thr Gly Ser 30 35 40 45			147
gaa gta tca tct gtc ttc atc ttc ccc cca aag ccc aaa gat gtg ctc Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu 50 55 60			195
acc atc act ctg act cct aag gtc acg tgt gtt gtg gta gac att agc Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser 65 70 75			243
cag gac gat ccc gag gtc cat ttc agc tgg ttt gta gat gac gtg gaa Gln Asp Asp Pro Glu Val His Phe Ser Trp Phe Val Asp Asp Val Glu 80 85 90			291
gtc cac aca gct cag act cga cca cca gag gag cag ttc aac agc act Val His Thr Ala Gln Thr Arg Pro Pro Glu Glu Gln Phe Asn Ser Thr 95 100 105			339
ttc cgc tca gtc agt gaa ctc ccc atc ctg cac cag gac tgg ctc aat Phe Arg Ser Val Ser Glu Leu Pro Ile Leu His Gln Asp Trp Leu Asn 110 115 120			387

ggc agg acg ttc aga tgc aag gtc acc agt gca gct ttc cca tcc ccc		435	
Gly Arg Thr Phe Arg Cys Lys Val Thr Ser Ala Ala Phe Pro Ser Pro			
130	135	140	
atc gag aaa acc atc tcc aaa ccc gaa ggc aga aca caa gtt ccg cat		483	
Ile Glu Lys Thr Ile Ser Lys Pro Glu Gly Arg Thr Gln Val Pro His			
145	150	155	
gta tac acc atg tca cct acc aag gaa gag atg acc cag aat gaa gtc		531	
Val Tyr Thr Met Ser Pro Thr Lys Glu Glu Met Thr Gln Asn Glu Val			
160	165	170	
agt atc acc tgc atg gta aaa ggc ttc tat ccc cca gac att tat gtg		579	
Ser Ile Thr Cys Met Val Lys Gly Phe Tyr Pro Pro Asp Ile Tyr Val			
175	180	185	
gag tgg cag atg aac ggg cag cca cag gaa aac tac aag aac act cca		627	
Glu Trp Gln Met Asn Gly Gln Pro Gln Glu Asn Tyr Lys Asn Thr Pro			
190	195	200	205
cct acg atg gac aca gat ggg agt tac ttc ctc tac agc aag ctc aat		675	
Pro Thr Met Asp Thr Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Asn			
210	215	220	
gtg aag aag gaa aaa tgg cag cag gga aac acg ttc acg tgt tct gtg		723	
Val Lys Lys Glu Lys Trp Gln Gln Gly Asn Thr Phe Thr Cys Ser Val			
225	230	235	
ctg cat gaa ggc ctg cac aac cac cat act gag aag agt ctc tcc cac		771	
Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His			
240	245	250	
tct ccg ggt aaa gcc caa gat ttt gtg cag tgg ttg atg aat acc		816	
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ctc ctt ctc atc ctt ctg ttt cat tca gag gca gcc tgc cgc cct tct		99
Leu Leu Leu Ile Leu Leu Phe His Ser Glu Ala Ala Cys Arg Pro Ser		
15	20	25
ggg aaa aga ccc tgc aag atg caa gcc ttc aga atc tgg gat act aac		147
Gly Lys Arg Pro Cys Lys Met Gln Ala Phe Arg Ile Trp Asp Thr Asn		
30	35	40
45		
cag aag acc ttt tac ctg aga aac aac cag ctc att gct ggg tac tta		195
Gln Lys Thr Phe Tyr Leu Arg Asn Asn Gln Leu Ile Ala Gly Tyr Leu		
50	55	60
caa gga cca aat atc aaa cta gaa gaa aag ata gac atg gtg cct att		243
Gln Gly Pro Asn Ile Lys Leu Glu Glu Lys Ile Asp Met Val Pro Ile		
65	70	75
gac ctt cat agt gtg ttc ttg ggc atc cac ggg ggc aag ctg tgc ctg		291
Asp Leu His Ser Val Phe Leu Gly Ile His Gly Gly Lys Leu Cys Leu		
80	85	90
tct tgt gcc aag tct gga gat gat atc aag ctc cag ctg gag gaa gtt		339
Ser Cys Ala Lys Ser Gly Asp Asp Ile Lys Leu Gln Leu Glu Glu Val		
95	100	105
aac atc act gat ctg agc aag aac aaa gaa gaa gac aag cgc ttt acc		387
Asn Ile Thr Asp Leu Ser Lys Asn Lys Glu Glu Asp Lys Arg Phe Thr		
110	115	120
125		
ttc atc cgc tct gag aaa ggc ccc acc acc agc ttt gag tca gct gcc		435
Phe Ile Arg Ser Glu Lys Gly Pro Thr Thr Ser Phe Glu Ser Ala Ala		
130	135	140
tgt cca gga tgg ttc ctc tgc aca aca cta gag gct gac cgt cct gtg		483
Cys Pro Gly Trp Phe Leu Cys Thr Thr Leu Glu Ala Asp Arg Pro Val		
145	150	155
agc ctc acc aac aca ccg gaa gag ccc ctt ata gtc acg aag ttc tac		531
Ser Leu Thr Asn Thr Pro Glu Glu Pro Leu Ile Val Thr Lys Phe Tyr		
160	165	170
ttc cag gaa gac caa gcg gcc gcc gtg ccc aga aac tgt gga ggt gat		579
Phe Gln Glu Asp Gln Ala Ala Val Pro Arg Asn Cys Gly Gly Asp		
175	180	185
tgc aag cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc		627
Cys Lys Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile		
190	195	200
205		
ttc ccc cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag		675
Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys		
210	215	220
gtc acg tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat		723
Val Thr Cys Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His		

225	230	235	
ttc agc tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg 240	245	250	771
cca cca gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc Pro Pro Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu 255	260	265	819
ccc atc ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag Pro Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys 270	275	280	867
gtc acc agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa Val Thr Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys 290	295	300	915
ccc gaa ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc Pro Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr 305	310	315	963
aag gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa Lys Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys 320	325	330	1011
ggc ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag Gly Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln 335	340	345	1059
cca cag gaa aac tac aag aac act cca cct acg atg gac aca gat ggg Pro Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly 350	355	360	1107
agt tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag Ser Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Glu Lys Trp Gln 370	375	380	1155
cag gga aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac Gln Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn 385	390	395	1203
cac cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp 400	405	410	1251
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51

ctg att tct gca gct ctg tgt gaa ggt gca gtt ttg cca agg agt gct
Leu Ile Ser Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala
15 20 25

99

aaa gaa ctt aga tgt cag tgc ata aag aca tac tcc aaa cct ttc cac
Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His
30 35 40 45

147

ccc aaa ttt atc aaa gaa ctg aga gtg att gag agt gga cca cac tgc
Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys
50 55 60

195

gcc aac aca gaa att att gta aag ctt tct gat gga aga gag ctc tgt
Ala Asn Thr Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys
65 70 75

243

ctg gac ccc aag gaa aac tgg gtg cag agg gtt gtg gag aag ttt ttg
Leu Asp Pro Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu
80 85 90

291

aag agg gct gag aat tca gcg gcc gcc ccg ggt aaa gcc caa gat ttt
Lys Arg Ala Glu Asn Ser Ala Ala Pro Gly Lys Ala Gln Asp Phe
95 100 105

339

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369

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